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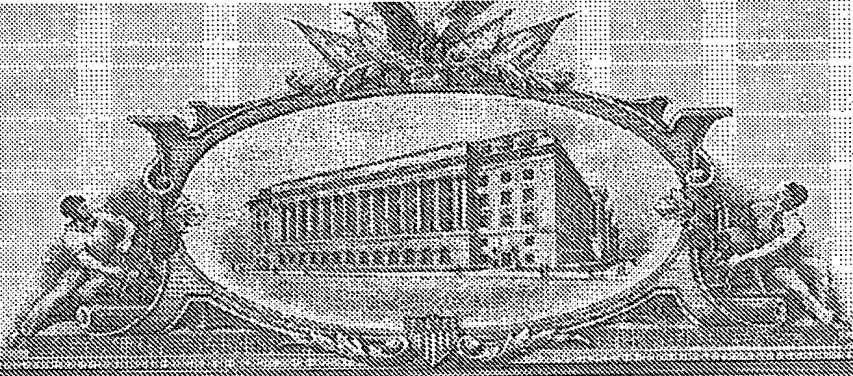
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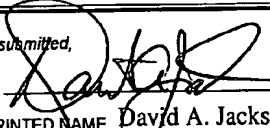
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Additional inventors are being named on the _____ separately numbered sheets attached hereto		
TITLE OF THE INVENTION (500 characters max)		
MAPK DETECTION METHOD FOR HETEROGENEOUS TISSUES		
CORRESPONDENCE ADDRESS		
Direct all correspondence to:		
<input checked="" type="checkbox"/> Customer Number	23565	Place Customer Number Bar Code Label here
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ENCLOSED APPLICATION PARTS (check all that apply)		
<input checked="" type="checkbox"/> Specification Number of Pages	57	<input type="checkbox"/> CD(s), Number
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METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT		
<input checked="" type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27.	FILING FEE AMOUNT (\$)	
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<input checked="" type="checkbox"/> The Director is hereby authorized to charge filing fees or credit any overpayment to Deposit Account Number.	11-153	\$80.00
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[Page 1 of 2]

Respectfully submitted,
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Date 6/19/03
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601-1-132P

DETECTION OF MUTATIONS IN NUCLEIC ACID SEQUENCES

TECHNICAL FIELD

The present invention pertains to the fields of molecular biology and diagnostic medicine. More specifically, the invention relates to methods for distinguishing a mutant allele comprising a mutation from a corresponding wild type allele or other allele lacking the specific mutation. For some applications, the method of the invention may be used to distinguish a mutant allele having oncogenic properties, such as an oncogene or proto-oncogene, from an allele lacking the mutation that confers oncogenic properties.

BACKGROUND OF THE INVENTION

Several publications and patent documents are referenced in this application in order to more fully describe the state of the art to which this invention pertains. The disclosure of each of these publications and documents is incorporated by reference herein.

The detection of mutations in DNA is of significant importance in a variety of fields, particularly with regard to diagnostic and prognostic applications. The diagnosis of genetically determined diseases and identification of disease carriers, for example, relies in large part on the identification of DNA mutations associated with the disease in individuals. Indeed, in Northern Europe diseases caused by genetically determined defects may affect 1% of all live births. In some Mediterranean countries, 20% of the population is predicted to have a genetic defect associated with thalassaemia. Moreover, many cancers are known to be associated with or caused by a mutation in a nucleic acid sequence. Such mutations generally involve a monobasic substitution. A number of methods have been proposed for detecting such mutations. Some of the methods shall now be illustrated.

Conventional methods of gene analysis involve DNA isolation and restriction digestion, gel electrophoresis and Southern DNA blotting, hybridization with radioactive probes and washing, and finally autoradiography. Several days are required for this process. Such methods are the subject of a review by Little in "Genetic Engineering" volume 1, pages 61-102, 1981, Academic Press.

Such methods can be used whether or not the DNA has been accurately sequenced in the region of interest. But this approach has major disadvantages, including the ability to detect point mutations only when present in a restriction enzyme cleavage site, and then only when other cleavage sites for the same enzyme are not present within the general vicinity; and the requirement for the lengthy preliminary steps of DNA isolation, restriction, gel electrophoresis, and Southern blotting. These disadvantages have inhibited the use of these techniques for genetic screening in clinical laboratories.

When the DNA sequence in the region of interest is known, it is possible to overcome some of these disadvantages. Conner et al. (Proc. Natl. Acad. Sci. U.S.A., 80, 1983, 278-282) describe a method which does not require the mutation to be located within a restriction enzyme cleavage site. A radioactively-labeled oligonucleotide probe is hybridized to the region of the DNA which includes the possible mutation. The hybridization conditions are empirically determined to optimize differential hybridization of the probe to a nucleic acid sequence with the mutation, as opposed to a nucleic acid sequence lacking the mutation. The length of the probe and the hybridization conditions are also experimentally determined, the optimization of which is difficult and critical for success. The necessity of using a radioactively labeled probe and the aforementioned tedious preliminary steps render this method of limited utility.

DNA (RNA) sequencing may also be used to determine the nucleic acid sequence of a molecule suspected or known to be associated with a disease state or disorder. Although nucleic acid sequencing is very reliable, it is prohibitively expensive and involves multiple procedural steps requiring a high degree of technical expertise for execution.

A DNA chip wherein a number of oligonucleotides are fixed onto a glass surface and selectively hybridized with a substance to be analyzed (e.g., a DNA fragment comprising a mutation) may be used to detect a signal (e.g., a fluorescent signal) that reveals hybridization of the substance to the chip. Comparison of this signal with that produced by hybridization to a "normal substance" (e.g., a DNA fragment which does not comprise the mutation) provides means to estimate the sequence of the substance. The cost of such DNA chips, however, is prohibitive. Moreover, the number of oligonucleotides fixed onto the chip must be varied according to the substance, which further amplifies methodological expenses.

In the SSCP (Single Strand Conformation Polymorphism) method, double stranded nucleic acid sequence (DNA or RNA) is dissociated into single stranded nucleic acid sequence and the higher-order structure of the single stranded nucleic acid sequence may be determined by, for example, polyacrylamide gel electrophoresis. A specific higher-order structure of a single stranded nucleic acid sequence is dependent on the nucleic acid sequence of the molecule and, thus, a difference of a single nucleotide in a molecule is detectable as a change in the mobility of the molecule in a polyacrylamide gel following electrophoresis. SSCP, therefore, provides a means to estimate the presence/absence of a monobasic substitution. The SSCP method, however, requires detailed analysis of optimal electrophoretic conditions for each sample, a process which is tedious and cumbersome and, therefore, not amenable to high throughput analyses.

In the DGGE (Denaturing Gradient Gel Electrophoresis) method, a sample comprising a PCR (polymerase chain reaction) product is separated by electrophoresis in a polyacrylamide gel with a concentration gradient of a denaturant optimized for comparing the dissociation of different DNA molecules from double stranded to single stranded DNA. A difference of a single base pair may, therefore, be detected using this method. The DGGE method, however, requires detailed analysis of the optimal composition of the electrophoretic gel for each sample, an involved process that is not amenable to high throughput analyses.

In the DHPLC (Denaturing High Performance Liquid Chromatography) method, a sample of double stranded DNA and a standard double stranded DNA (i.e., a double stranded DNA with a known base sequence, such as a wild type DNA) are mixed, thermally denatured to be dissociated into single stranded DNA, and thereafter cooled to reanneal the single stranded DNA to become double stranded DNA. When a sample includes only double stranded DNA with a standard base sequence, only a homoduplex is formed. When a sample includes a double stranded DNA with a monobasic substitution in addition to the standard double stranded DNA, homoduplexes and heteroduplexes having a mismatch site formed at the site of the substitution are formed. A heteroduplex has a smaller number of hydrogen bonds formed than a homoduplex, as a consequence of the presence of the mismatch. The heteroduplex may, therefore, be detected using high-speed liquid chromatography which can differentiate molecules based on distinct melting temperatures (i.e., T_m : temperature at which 50% of the total concentration of double stranded DNA is denatured to single stranded DNA). Of note, the T_m of the heteroduplex is lower than that of the homoduplex, and may be distinguished on this basis. The DHPLC method, however, is expensive due to the cost involved with liquid chromatography.

SUMMARY OF THE INVENTION

The present invention is directed to a method for detecting a mutation in a target nucleic acid sequence, said method comprising:

- (a) providing a plurality of nucleic acid sequences comprising said target nucleic acid sequence, wherein said mutation is located in a first portion of a restriction endonuclease site;
- (b) providing a first primer hybridizable to said target nucleic acid sequence, said first primer comprising a second portion of said restriction endonuclease site, and a second primer hybridizable to said target nucleic acid sequence, wherein said first and second primer comprise a polymerase chain reaction (PCR) primer pair;

- (c) performing a PCR amplification of said plurality of nucleic acid sequences using said PCR primer pair, wherein said PCR amplification produces a target nucleic acid sequence amplicon comprising a site recognizable by a restriction endonuclease in the presence of said mutation, said site comprising the first portion and second portion of said restriction endonuclease site, said first portion and second portion of said restriction endonuclease site operably linked by said PCR amplification;
- (d) incubating PCR amplicons produced in step (c) with said restriction endonuclease capable of recognizing said restriction endonuclease site under conditions permissible for said restriction endonuclease activity; and
- (e) detecting nucleic acid fragments produced in step (d), wherein detection of a pattern of nucleic acid fragments is indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by said restriction endonuclease,

said pattern of nucleic acid fragments being indicative of a presence of a mutation in said target nucleic acid sequence in said plurality of nucleic acid sequences.

In accordance with the method of the present invention, a target nucleic acid sequence can be an allele associated with a disorder, an oncogene, or a proto-oncogene. Such target nucleic acid sequences are isolated from a biological sample, such as, for example, a patient sample.

In one aspect of the method of the invention, the presence of a mutation in a target nucleic acid sequence is indicative of a disorder. Such disorders include, but are not limited to genetic diseases, metabolic diseases, and hyperproliferative diseases. An

example of a hyperproliferative disease diagnosable using the method of the invention is a cancer.

In another aspect of the method of the invention, the presence of a mutation in a target nucleic acid sequence is indicative of a predisposition to a disorder. Such disorders include, but are not limited to genetic diseases, metabolic diseases, and hyperproliferative diseases. A predisposition to a hyperproliferative disease such as a cancer, for example, is determinable using the method of the invention.

In one embodiment, the method of the invention is used to detect a mutation in an oncogene which is an activating point mutation. Such mutations occur in a number of genetic alleles including, but not limited to, a *B-RAF* allele and an *N-RAS* allele.

In an aspect of the invention, the method is used to detect a *B-RAF* allele encoding a mutated *B-RAF* polypeptide comprising a V599E mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 7 and a second primer SEQ ID NO: 8 is used to amplify amplicons from the mutated *B-RAF* allele/template. Such amplicons comprise an Alw26 I restriction endonuclease site. Digestion of amplicons generated from a mutated *B-RAF* allele with Alw26 I produces a pattern of nucleic acid fragments, including fragments of 123 and 37 base pairs. Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

In another aspect of the invention, the method is used to detect an *N-RAS* allele encoding a mutated *N-RAS* polypeptide comprising a Q61R mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 9 and a second primer SEQ ID NO: 10 is used to amplify amplicons from the mutated *N-RAS* allele/template. Such amplicons comprise a Bcg I restriction endonuclease site. Digestion of amplicons generated from such a mutated *N-RAS* allele with Bcg I produces a pattern of nucleic acid fragments, including fragments of 168, 34, and 22 base pairs.

Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

In another aspect of the invention, the method is used to detect an *N-RAS* allele encoding a mutated *N-RAS* polypeptide comprising a Q61K mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 11 and a second primer SEQ ID NO: 12 is used to amplify amplicons from the mutated *N-RAS* allele/template. Such amplicons comprise an Sfu I restriction endonuclease site. Digestion of amplicons generated from such a mutated *N-RAS* allele with Sfu I produces a pattern of nucleic acid fragments, including fragments of 210 and 40 base pairs. Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

Also presented is a method for detecting a mutation in a target nucleic acid sequence, said method comprising incorporating a restriction enzyme site into a target nucleic acid sequence amplicon, wherein said incorporating is effectuated by polymerase chain reaction (PCR) of a target nucleic acid sequence comprising a mutation, wherein said restriction enzyme site incorporated by PCR comprises said mutation in said target nucleic acid sequence amplicon, and said target nucleic acid sequence amplicon comprising the restriction enzyme site is digestable by said restriction enzyme, and digesting with said restriction enzyme produces a pattern of nucleic acid fragments indicative of a presence of a target nucleic acid sequence comprising a mutation.

The present invention is further directed to a method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence, said method comprising:

- (a) providing a plurality of nucleic acid sequences comprising said target nucleic acid sequence, wherein said mutation is located in a first portion of a restriction endonuclease site;
- (b) providing a first primer hybridizable to said target nucleic acid sequence, said first primer comprising a second portion of said

restriction endonuclease site, and a second primer hybridizable to said target nucleic acid sequence, wherein said first and second primer comprise a polymerase chain reaction (PCR) primer pair;

(c) performing a PCR amplification of said plurality of nucleic acid sequences using said PCR primer pair, wherein said PCR amplification produces a target nucleic acid sequence amplicon comprising a site recognizable by a restriction endonuclease in the presence of said mutation, said site comprising the first portion and second portion of said restriction endonuclease site, said first portion and second portion of said restriction endonuclease site operably linked by said PCR amplification;

(d) incubating PCR amplicons produced in step (c) with said restriction endonuclease capable of recognizing said restriction endonuclease site under conditions permissible for said restriction endonuclease activity; and

(e) detecting nucleic acid fragments produced in step (d), wherein detection of a pattern of nucleic acid fragments is indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by said restriction endonuclease,

said pattern of nucleic acid fragments being indicative of a presence of a mutation in said target nucleic acid sequence in said plurality of nucleic acid sequences, wherein said presence of said mutation is a positive diagnostic indicator of a disorder associated with said mutation in said target nucleic acid sequence.

In accordance with the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence, a target nucleic acid sequence can be an allele associated with a disorder, an oncogene, or a proto-oncogene. Such target nucleic acid sequences are isolated from a biological sample, such as, for example, a patient sample.

In one aspect of the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence, the presence of a mutation in a target nucleic acid sequence is indicative of the disorder. Such disorders include, but are not limited to genetic diseases, metabolic diseases, and hyperproliferative diseases. An example of a hyperproliferative disease diagnosable using the method of the invention is a cancer.

In another aspect of the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence, the presence of a mutation in a target nucleic acid sequence is indicative of a predisposition to a disorder. Such disorders include, but are not limited to genetic diseases, metabolic diseases, and hyperproliferative diseases. A predisposition to a hyperproliferative disease such as a cancer, for example, is determinable using the method of the invention.

In one embodiment, the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence is used to detect a mutation in an oncogene which is an activating point mutation. Such mutations occur in a number of genetic alleles including, but not limited to, a *B-RAF* allele and an *N-RAS* allele.

In an aspect of the invention, the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence is used to detect a *B-RAF* allele encoding a mutated *B-RAF* polypeptide comprising a V599E mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 7 and a second primer SEQ ID NO: 8 is used to amplify amplicons from the mutated *B-RAF* allele/template. Such amplicons comprise an Alw26 I restriction endonuclease site. Digestion of amplicons generated from a mutated *B-RAF* allele with Alw26 I produces a pattern of nucleic acid fragments, including fragments of 123 and 37 base pairs. Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

In another aspect of the invention, the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence is used to detect an *N-RAS* allele encoding a mutated *N-RAS* polypeptide comprising a Q61R mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 9 and a second primer SEQ ID NO: 10 is used to amplify amplicons from the mutated *N-RAS* allele/template. Such amplicons comprise a Bcg I restriction endonuclease site. Digestion of amplicons generated from such a mutated *N-RAS* allele with Bcg I produces a pattern of nucleic acid fragments, including fragments of 168, 34, and 22 base pairs. Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

In another aspect of the invention, the method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence is used to detect an *N-RAS* allele encoding a mutated *N-RAS* polypeptide comprising a Q61K mutation. In accordance with the method of the invention, a PCR primer pair comprising a first primer SEQ ID NO: 11 and a second primer SEQ ID NO: 12 is used to amplify amplicons from the mutated *N-RAS* allele/template. Such amplicons comprise an Sfu I restriction endonuclease site. Digestion of amplicons generated from such a mutated *N-RAS* allele with Sfu I produces a pattern of nucleic acid fragments, including fragments of 210 and 40 base pairs. Detection of this diagnostic pattern of nucleic acid fragments provides a positive indicator of melanoma.

As described herein, the methods of the present invention are useful for detecting a mutation associated with disease and for diagnosing a disease. An exemplary disease diagnosable using the methods of the invention is melanoma. The present invention also provides a method for indicating melanoma disease progression or the clinical stage of the disease.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A, 1B, and 1C show nucleic acid sequences depicting the creation of an Alw26 I restriction site near codon 1796 of *B-RAF* having the V599E mutation, the novel

restriction enzyme digestion pattern predicted for a PCR product comprising the novel site, and a photograph of an agarose gel of digested PCR products following electrophoresis, respectively.

Figures 2A, 2B, and 2C show nucleic acid sequences depicting the creation of a Bcg I restriction site near codon 61 of *N-RAS* with a guanine (arrow) replacing an adenine to form the Q61R mutation, the novel restriction enzyme digestion pattern predicted for a PCR product comprising the novel site, and a photograph of an agarose gel of digested PCR products following electrophoresis, respectively.

Figures 3A, 3B, and 3C show nucleic acid sequences depicting the creation of an Sfu I restriction site near codon 61 of *N-RAS* with an adenine (arrow) replacing a cytosine to form the Q61K mutation, the novel restriction enzyme digestion pattern predicted for a PCR product comprising the novel site, and a photograph of an agarose gel of digested PCR products following electrophoresis, respectively.

Figure 4 shows a photograph of an agarose gel following electrophoresis, wherein serially diluted plasmids containing the V599E mutant sequence were analyzed.

Figures 5 A and 5B show immunoblots of cellular extracts probed with antibodies immunologically specific for ERK 1/2, phosphorylated ERK 1/2, or phosphorylated MEK 1/2.

DETAILED DESCRIPTION OF THE INVENTION

The method of the present invention is directed to detecting a difference in the sequence of two related nucleic acid sequences. Such differences relate to any mutation including, but not limited to a single base substitution, deletion or insertion within a sequence which can be specifically recognized by a primer suitable for use in a polymerase chain reaction. The method is applicable to the detection of a known mutation in any biological sample on which PCR may be performed. The method is simple, fast and amenable to

automation. It is ideally suited for analysis of patient samples and rapid mutation pre-screening.

A large number of mutations in complex eukaryotic genes comprising a plurality of exons that encode large polypeptides have been shown to be clinically significant. Mutations in such genes have been implicated in a variety of genetic disorders and have been associated with a predisposition for and/or onset of a disease (e.g., cancer). Improved methods for detecting mutations and polymorphisms in such genes are, therefore, needed. In particular, there is a need for methods that can use either DNA or RNA as starting material. Previously described techniques include restriction endonuclease fingerprinting (REF), the single-stranded conformation polymorphism (SSCP) technique, and the protein truncation test (PTT). See above for more detail pertaining to these techniques and impediments to their use. There is also a need for a method that can detect a mutation in a non-coding region of a gene, wherein control elements are frequently located, which could be undetectable using some of the above techniques. Thus, there is a need for improved methods for detecting mutations and polymorphisms in eukaryotic genes, including complex eukaryotic genes. As described herein, the method of the present invention addresses this need.

In one embodiment, the method of the present invention was used successfully to screen a large sample of melanoma samples (N=85) for the presence of the most common *B-RAF* and *N-RAS* mutations associated with melanoma. Recent studies have suggested that activating point mutations in *B-RAF* may commonly occur in melanoma and therefore, detection of such mutations would provide a positive indicator of melanoma. Accordingly, as described herein, a method to detect point mutations in heterogeneous tissues containing both wild-type and mutant *B-RAF* and *N-RAS* genes was devised which utilizes site-directed mutagenesis to introduce a new restriction site into a PCR amplicon derived from a template in which a specific point mutation is present (a target nucleic acid sequence). Thus, the presence of a newly incorporated restriction enzyme site into amplicons generated from a mutated template provides a positive indicator for the

presence of a mutated template in a heterogeneous population of templates and therefore provides means to detect the mutation.

As presented herein, the method of the invention was used to determine the incidence of mutations in components of mitogen-activated protein kinase (MAPK) pathways in human melanoma. Moreover, corroborative techniques such as immunoblotting (Western blotting) were also used to evaluate and demonstrate downstream up-regulation of MAPK pathways in these tissues.

Of the 85 samples evaluated using the present method, thirty-three samples (7 of 25 primaries, 15 of 25 regional metastases, 5 of 25 nodal metastases, and 6 of 10 distant metastases) harbored the V599E *B-RAF* mutation (39 %), twelve comprised a Q61R *N-RAS* mutation and five comprised a Q61K *N-RAS* mutation. Western blotting with anti-phosphorylated ERK 1/2 antibodies demonstrated up-regulation of the MAPK pathway in samples containing activating *B-RAF* or *N-RAS* mutations, as compared with MAPK pathway activity in wild-type samples. Of note, there were no false positives detected since the presence of an activating mutation in the MAPK pathway in a sample was confirmed by downstream activation of the pathway in the sample. The method of the invention, therefore, provides a rapid, sensitive, and specific means for detecting a mutation in a biological sample.

As shown herein using the methods of the present invention, activating mutations of the MAPK pathway were present in approximately 60% of samples tested and caused activation of this cellular pathway. These findings underscore the significance of MAPK pathway activation in the diagnosis and pathogenesis of melanoma.

The method of the present invention for detecting/identifying point mutations, which utilizes a modified site-directed mutagenesis approach, can also be used to detect non-MAPK related mutations. Indeed, any known monobasic mutation is detectable using the method of the present invention. The method of the present invention may, for example, be used to advantage for detecting inactivating point mutations in the BRCA2 gene that

are associated with a very high incidence of breast cancer. Multiple point mutations, insertions, and deletions in the BRCA1 and BRCA 2 genes result in the inactivation of these genes. Currently, if a patient with breast cancer is found to harbor a mutation in one of the BRCA genes, family members are routinely screened to determine if they also harbor a mutation in either BRCA 1 or BRCA 2. The presence of such mutations provides a strong positive indicator of a predisposition of an individual for developing breast cancer. The method of the present invention can, therefore, be used to identify individuals at risk for breast cancer, who should be monitored and examined at a greater frequency than patients lacking such mutations. Such individuals may also be treated prophylactically with a variety of prophylactic/therapeutics compounds known to skilled practitioners.

Practicing the method of the present invention for the detection of BRCA2 mutations is assisted by the availability of the full length sequence of the BRCA2 gene and characterization of a number of clinically significant mutations in chromosome 13q-linked kindreds. See Tavtigian et al. Nature Genetics, 1996;12(3):333. Screening methods presently employed to detect BRCA mutations involve sequencing of family member's BRCA genes, the nucleic acid sequences of which are generally isolated from a peripheral blood sample. Such methods are expensive and time consuming. Once a mutation has been characterized by sequencing the original patient's BRCA genes, however, the method of the present invention may be used to detect this specific mutation (and/or other BRCA gene mutations) in other family members. Moreover, because inactivating mutations in the BRCA genes are generally germ-line mutations, the family members are anticipated to harbor the same mutation as the index or original patient.

One of ordinary skill in the art could, therefore, in accordance with the method of the present invention, design a specific set of primers or a PCR primer pair capable of incorporating a new diagnostic restriction enzyme site into a PCR amplicon derived from a BRCA gene comprising such a mutation. The presence of the diagnostic restriction enzyme site in PCR amplicons, as revealed by successful digestion of such amplicons with the specific restriction enzyme would, therefore, be indicative of a presence of the

mutated BRCA gene in a patient sample. Thus, the present invention provides a relatively simple, inexpensive, and accurate method for screening large numbers of family members related to patients diagnosed as having a mutation in a BRCA gene.

An ordinarily skilled practitioner could readily apply the method of the present invention to a characterized mutation in any allele or gene. Indeed, all that is required to practice the present method is knowledge pertaining to the nucleic acid sequence of a mutated site and the nucleic acid sequences flanking the mutation in question. With such information and in accordance with the invention, an ordinarily skilled artisan could readily design a specific PCR primer pair to incorporate a diagnostic restriction enzyme site into a PCR amplicon generated from a template comprising a mutation in question, perform a PCR amplification to produce PCR amplicons, and analyze the resultant nucleic acid fragments produced to determine if a template comprising the mutation is present in a sample.

In order to more clearly set forth the parameters of the present invention, the following definitions are used:

As used in the specification and appended claims, the singular forms "a", "an", and "the" include plural references unless the context clearly dictates otherwise. Thus for example, reference to "the method" includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure and so forth.

The phrase "flanking nucleic acid sequences" refers to those contiguous nucleic acid sequences that are 5' and 3' to a particular nucleic acid (e.g., a point mutation) or stretch of nucleic acid sequences (e.g., an endonuclease cleavage site).

The term "restriction endonuclease" refers to an enzyme that can cleave DNA internally.

The term "complementary" refers to two DNA strands that exhibit substantial normal base

pairing characteristics. Complementary DNA may, however, contain one or more mismatches.

The term "hybridization" refers to the hydrogen bonding that occurs between two complementary DNA strands.

The term "specifically hybridize" refers to the association between two single-stranded nucleic acid molecules of sufficiently complementary sequence to permit such hybridization under pre-determined conditions generally used in the art (sometimes termed "substantially complementary"). In particular, the term refers to hybridization of an oligonucleotide with a substantially complementary sequence contained within a single-stranded DNA or RNA molecule of the invention, to the substantial exclusion of hybridization of the oligonucleotide with single-stranded nucleic acids of non-complementary sequence.

The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG software program and are known in the art.

As used herein, a "nucleic acid" is a compound or composition that is a polymeric nucleotide or polynucleotide. Nucleic acids include both nucleic acids and fragments thereof from any source, in purified or unpurified form, including DNA (dsDNA and ssDNA) and RNA (e.g., t-RNA, m-RNA, r-RNA), mitochondrial DNA and RNA, chloroplast DNA and RNA, DNA-RNA hybrids, or mixtures thereof, genes, chromosomes, plasmids, the genomes of biological material such as microorganisms, e.g., bacteria, yeasts, viruses, viroids, molds, fungi, plants, animals, and humans. Sequences of interest may be embedded in sequences of any length of, for example, a chromosome, cDNA, or plasmid. The nucleic acid may be only a minor fraction of a complex mixture such as that of a biological sample. The nucleic acid may be obtained from a biological sample by procedures well known in the art.

With reference to nucleic acids of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA molecule that is separated from sequences with which it is immediately contiguous in the naturally occurring genome of the organism in which it originated. For example, an "isolated nucleic acid" may comprise a DNA molecule inserted into a vector, such as a plasmid or virus vector, or integrated into the genomic DNA of a prokaryotic or eukaryotic cell or host organism.

In applications wherein the nucleic acid is RNA, it may first be converted to cDNA by means of a primer and reverse transcriptase. The nucleotide polymerase used in the present invention for carrying out amplification and chain extension can have reverse transcriptase activity. A nucleic acid sequence may comprise a particular gene or mutant thereof of biological interest such as, for example, the hemoglobin gene associated with sickle-cell anemia, the cystic fibrosis gene, and a number of oncogenes and proto-oncogenes.

When applied to RNA, the term "isolated nucleic acid" refers primarily to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively, the term may refer to an RNA molecule that has been sufficiently separated from other nucleic acids with which it is generally associated in its natural state (i.e., in cells or tissues). An isolated nucleic acid (either DNA or RNA) may further represent a molecule produced directly by biological or synthetic means and separated from other components present during its production.

As used herein, a "sample" refers to a material suspected of containing a nucleic acid. Such samples include, but are not limited to biological fluids such as blood, serum, plasma, sputum, lymphatic fluid, semen, vaginal mucus, feces, urine, spinal fluid and amniotic fluid; and biological tissue such as a tumor sample (excised or aspirated, e.g.) or hair and skin. Other samples include cell cultures and the like, plants, food, forensic samples such as paper, fabrics and scrapings, water, sewage, and medicinals. When necessary, the sample may be pretreated with reagents to liquefy the sample and release

the nucleic acids from binding substances. Such pretreatments are well known in the art.

As used herein, "amplification of nucleic acids" refers to any method that results in the formation of one or more copies of a nucleic acid (exponential amplification). One such method for enzymatic amplification of specific sequences of DNA is known as the polymerase chain reaction (PCR), as described by Saiki et al. (1986) *Science*, 230: 1350-1354. This *in vitro* amplification procedure is based on repeated cycles of denaturation, oligonucleotide primer annealing, and primer extension by a thermophilic template dependent polynucleotide polymerase, resulting in an exponential increase in copies of the desired sequence of the nucleic acid flanked by the primers. The two different PCR primers are designed to anneal to opposite strands of the DNA at positions that allow the polymerase catalyzed extension product of one primer to serve as a template strand for the other, leading to the accumulation of a discrete double stranded fragment whose length is defined by the distance between the 5' ends of the oligonucleotide primers. Primer length can vary from about 10 to 50 or more nucleotides and primers are usually selected to be at least about 15 nucleotides to ensure high specificity. The double stranded fragment that is produced is called an "amplicon" and may vary in length from as few as about 30 nucleotides to 10,000 or more.

As used herein, "chain extension of nucleic acids" refers to extension of the 3'-end of a polynucleotide in which additional nucleotides or bases are appended. Chain extension relevant to the present invention is template dependent, that is, the appended nucleotides are determined by the sequence of a template nucleic acid to which the extending chain is hybridized. The chain extension product sequence that is produced is complementary to the template sequence. Usually, chain extension is enzyme catalyzed, preferably, in the present invention, by a thermophilic DNA polymerase.

As used herein, "target nucleic acid sequence" refers to a sequence of nucleotides to be studied either for the presence of a difference from a related sequence or for the determination of its presence or absence. The target nucleic acid sequence may be double stranded or single stranded and from a natural or synthetic source. When the target

nucleic acid sequence is single stranded, the method of the present invention produces a nucleic acid duplex comprising the single stranded target nucleic acid sequence.

The target sequence usually exists within a portion or all of a nucleic acid, the identity of which is known to an extent sufficient to allow preparation of various primers necessary for introducing a restriction enzyme site into or near a target sequence or conducting an amplification of the target sequence or a chain extension of the products of such an amplification in accordance with the present invention. Accordingly, other than for the sites to which the primers bind, the identity of the target nucleic acid sequence may or may not be known. In general, in PCR, primers hybridize to, and are extended along (chain extended), a target sequence, and, thus, the target sequence acts as a template. The target sequence usually contains from about 30 to 20,000 or more nucleotides, more frequently, 100 to 10,000 nucleotides, preferably, 50 to 1,000 nucleotides. The target nucleic acid sequence is generally a fraction of a larger molecule or it may be substantially the entire molecule. The minimum number of nucleotides in the target sequence is selected to assure that a determination of a difference between two related nucleic acid sequences in accordance with the present invention can be achieved.

As used herein, a "reference nucleic acid sequence" refers to a nucleic acid sequence that is related to the target nucleic acid in that the two sequences are identical except for the presence of a difference, such as a mutation. Where a mutation is to be detected, the reference nucleic acid sequence usually contains the normal or "wild type" sequence. In certain situations the reference nucleic acid sequence may be part of a sample as, for example, in samples from tumors, the identification of partially mutated microorganisms, or identification of heterozygous carriers of a mutation. Consequently, both the reference and the target nucleic acid sequences are subjected to similar or the same amplification conditions. As with the target nucleic acid sequence, the identity of the reference nucleic acid sequence need be known only to an extent sufficient to allow preparation of various primers necessary for conducting an amplification of the reference sequence or a chain extension of the products of such amplification in accordance with the present invention.

Accordingly, other than for the sites to which the primers bind, the identity of the reference nucleic acid sequence may or may not be known.

The reference nucleic acid sequence may be a reagent employed in the methods of the present invention. Reference nucleic acid sequences are particularly useful in PCR amplification for detection of a target nucleic acid sequence. The reference nucleic acid reagent may be obtained from a natural source or prepared by known methods such as those described below in the definition of oligonucleotides.

As used herein, the phrase "related nucleic acid sequences" refers to two nucleic acid sequences that contain at least 15 nucleotides at each end that are identical but have different lengths or have intervening sequences that differ by at least one nucleotide. Frequently, related nucleic acid sequences differ from each other by a single nucleotide. Such a difference is referred to herein as the "difference between two related nucleic acid sequences." A difference can be produced by the substitution, deletion or insertion of any single nucleotide or a series of nucleotides within a sequence.

As used herein, a "mutation" refers to a change in the sequence of nucleotides of a normally conserved nucleic acid sequence resulting in the formation of a mutant as differentiated from the normal (unaltered) or wild type sequence. Mutations tend to be categorized into two general classes: base-pair substitutions and frameshift mutations. The latter entail the insertion or deletion of one to several nucleotide pairs. A difference of one nucleotide can be significant as to phenotypic normality or abnormality as in the case of, for example, sickle cell anemia.

As used herein, a "duplex" is a double stranded nucleic acid sequence wherein a majority of the nucleotides therein are complementary.

The term "oligonucleotide," as used herein refers to primers and probes of the present invention, and is defined as a nucleic acid molecule comprised of two or more ribo- or deoxyribonucleotides, preferably more than three. The exact size of the oligonucleotide

will depend on various factors and on the particular application for which the oligonucleotide is used.

Various techniques can be employed for preparing an oligonucleotide utilized in the present invention. Such oligonucleotides can be obtained by biological synthesis or by chemical synthesis. For short sequences (up to about 100 nucleotides), chemical synthesis will frequently be more economical as compared to biological synthesis. In addition to economy, chemical synthesis provides a convenient way of incorporating low molecular weight compounds and/or modified bases during the synthesis step. Furthermore, chemical synthesis is flexible with regard to the length and region of the target polynucleotide binding sequence. An oligonucleotide may be synthesized by standard methods such as those used in commercial automated nucleic acid synthesizers. Chemical synthesis of DNA on a suitably modified glass or resin can result in DNA covalently attached to the surface. This may offer advantages in washing and sample handling. For longer sequences, standard replication methods employed in molecular biology can be used such as the use of M13 for single stranded DNA as described by Messing (1983) *Methods Enzymol*, 101, 20-78.

Other methods of oligonucleotide synthesis include phosphotriester and phosphodiester methods (Narang et al. (1979) *Meth. Enzymol* 68: 90) and synthesis on a support (Beaucage et al. (1981) *Tetrahedron Letters* 22: 1859-1862) as well as the phosphoramidate technique, Caruthers et al., "Methods in Enzymology," Vol. 154, pp. 287-314 (1988), and others described in "Synthesis and Applications of DNA and RNA," Narang, editor, Academic Press, New York, 1987, and the references contained therein.

The term "primer" as used herein refers to an oligonucleotide, either RNA or DNA, either single-stranded or double-stranded, either derived from a biological system, generated by restriction enzyme digestion, or produced synthetically which, when placed in the proper environment, is able to act functionally as an initiator of template-dependent nucleic acid synthesis. When presented with an appropriate nucleic acid template, suitable nucleoside triphosphate precursors of nucleic acids, a polymerase enzyme, suitable cofactors and

conditions such as a suitable temperature and pH, the primer may be extended at its 3' terminus by the addition of nucleotides by the action of a polymerase or similar activity to yield a primer extension product. The primer may vary in length depending on the particular conditions and requirement of the application. For example, in diagnostic applications, the oligonucleotide primer is typically 15-25 or more nucleotides in length. The primer must be of sufficient complementarity to the desired template to prime the synthesis of the desired extension product, that is, to be able anneal with the desired template strand in a manner sufficient to provide the 3' hydroxyl moiety of the primer in appropriate juxtaposition for use in the initiation of synthesis by a polymerase or similar enzyme. It is not required that the primer sequence represent an exact complement of the desired template. For example, a non-complementary nucleotide sequence may be attached to the 5' end of an otherwise complementary primer. Alternatively, non-complementary bases may be interspersed within the oligonucleotide primer sequence, provided that the primer sequence has sufficient complementarity with the sequence of the desired template strand to functionally provide a template-primer complex for the synthesis of the extension product.

For applications wherein a primer is employed in a chain extension on a polynucleotide template such as in, for example, an amplification of a nucleic acid, the primer is usually a synthetic oligonucleotide that is single stranded and comprises a hybridizable sequence at its 3'-end that is capable of hybridizing with a defined sequence of the target or reference polynucleotide (nucleic acid sequence). In general, a hybridizable sequence of such a primer has at least 90%, preferably 95%, most preferably 100%, complementarity to a defined sequence or primer binding site. The number of nucleotides in the hybridizable sequence of an oligonucleotide primer should be such that stringency conditions used to hybridize the oligonucleotide primer will prevent excessive random non-specific hybridization. Usually, the number of nucleotides in the hybridizable sequence of the oligonucleotide primer will be at least ten nucleotides, preferably at least 15 nucleotides and, preferably 20 to 50, nucleotides.

The term "probe" as used herein refers to an oligonucleotide, polynucleotide or nucleic acid, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, which is capable of annealing with or specifically hybridizing to a nucleic acid with sequences complementary to the probe. A probe may be either single-stranded or double-stranded. The exact length of the probe will depend upon many factors, including temperature, source of probe and use of the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide probe typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The probes herein are selected to be "substantially" complementary to different strands of a particular target nucleic acid sequence. This means that the probes must be sufficiently complementary so as to be able to "specifically hybridize" or anneal with their respective target strands under a set of predetermined conditions. Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a non-complementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the sequence of the target nucleic acid to anneal therewith specifically.

The term "nucleoside triphosphates" refers to nucleosides having a 5'-triphosphate substituent. The nucleosides are pentose sugar derivatives of nitrogenous bases of either purine or pyrimidine derivation, covalently bonded to the 1'-carbon of the pentose sugar, which is usually a deoxyribose or a ribose. The purine bases comprise adenine(A), guanine (G), inosine (I), and derivatives and analogs thereof. The pyrimidine bases comprise cytosine (C), thymine (T), uracil (U), and derivatives and analogs thereof. Nucleoside triphosphates include deoxyribonucleoside triphosphates such as the four common triphosphates dATP, dCTP, dGTP and dTTP and ribonucleoside triphosphates such as the four common triphosphates rATP, rCTP, rGTP and rUTP.

The term "nucleoside triphosphates" also includes derivatives and analogs thereof, which

are exemplified by those derivatives that are recognized and polymerized in a similar manner to the underivatized nucleoside triphosphates. Examples of such derivatives or analogs, by way of illustration and not limitation, are those which are biotinylated, amine modified, alkylated, and the like and also include phosphorothioate, phosphite, ring atom modified derivatives, and the like.

The term "nucleotide" refers to a base-sugar-phosphate combination that is the monomeric unit of nucleic acid polymers, i.e., DNA and RNA.

The term "modified nucleotide" refers to a unit in a nucleic acid polymer that results from the incorporation of a modified nucleoside triphosphate during an amplification reaction and therefore becomes part of the nucleic acid polymer.

The term "nucleoside" refers to a base-sugar combination or a nucleotide lacking a phosphate moiety.

A "nucleotide polymerase" is a catalyst, usually an enzyme, for forming an extension of a polynucleotide along a DNA or RNA template wherein the extension is complementary thereto. The nucleotide polymerase is a template dependent polynucleotide polymerase and utilizes nucleoside triphosphates as building blocks for extending the 3'-end of a polynucleotide to provide a sequence complementary with the polynucleotide template. Usually, the catalysts are enzymes, such as DNA polymerases, for example, prokaryotic DNA polymerase (I, II, or III), T4 DNA polymerase, T7 DNA polymerase, Klenow fragment, and reverse transcriptase, and are preferably thermally stable DNA polymerases such as, for example, Vent® DNA polymerase, VentR® DNA polymerase, Pfu® DNA polymerase, and Taq® DNA polymerase, derived from any source such as cells, bacteria, such as *E. coli*, plants, animals, virus, and thermophilic bacteria.

The phrase "wholly or partially sequentially" refers to applications wherein the sample and various agents utilized in the present invention are combined other than concomitantly (simultaneously), one or more may be combined with one or more of the

remaining agents to form a subcombination. Subcombination and remaining agents can then be combined and can be subjected to the present method.

When used in the context of nucleotide sequences, "hybridization (hybridizing) or binding" are used interchangeably herein. The ability of two nucleotide sequences to hybridize to each other is based on the degree of complementarity of the nucleotide sequences, which in turn is based on the fraction of matched complementary nucleotide pairs. The degree of complementarity between two sequences is a significant factor to be considered with regard to the stringency of hybridization conditions utilizable and the specificity of the binding anticipated for the two sequences. Increased stringency is achieved by elevating the temperature, increasing the ratio of cosolvents, lowering the salt concentration, and the like.

"Complementary" refers to two sequences which can bind to each other in an anti-parallel sense wherein the 3'-end of each sequence binds to the 5'-end of the other sequence and each A, T(U), G, and C of one sequence is then aligned with a T(U), A, C, and G, respectively, of the other sequence.

A "copy" may, for example, refer to a sequence that is a direct identical copy of a single stranded polynucleotide sequence as differentiated from a sequence that is complementary to the sequence of such a single stranded polynucleotide.

As used herein, "conditions for extending a primer" includes a nucleotide polymerase, nucleoside triphosphates or analogs thereof capable of acting as substrates for the polymerase and other materials and conditions required for enzyme activity such as a divalent metal ion (usually magnesium), pH, ionic strength, organic solvent (such as formamide), and the like.

A member of a specific binding pair ("sbp member") refers to one of two different molecules, having an area on the surface or in a cavity which specifically binds to and is thereby defined as complementary with a particular spatial and polar organization of

another molecule. The members of the specific binding pair are referred to as ligand and receptor (antiligand). These may be members of an immunological pair such as antigen-antibody, or may be operator-repressor, nuclease-nucleotide, biotin-avidin, hormone-hormone receptor, IgG-protein A, DNA--DNA, DNA-RNA, and the like.

As used herein, "ligand" refers to any compound for which a receptor naturally exists or can be prepared.

As used herein, a "receptor" ("antiligand") refers to any compound or composition capable of recognizing a particular spatial and/or polar organization of a molecule, e.g., epitope or determinant site. Illustrative receptors include naturally occurring and synthetic receptors, e.g., thyroxine binding globulin, antibodies, enzymes, Fab fragments, lectins, nucleic acids, repressors, oligonucleotides, protein A, complement component C1q, or DNA binding proteins and the like.

As used herein, a "small organic molecule" refers to a compound of molecular weight less than about 1500, preferably 100 to 1000, more preferably 300 to 600 such as biotin, digoxigenin, fluorescein, rhodamine and other dyes, tetracycline and other protein binding molecules, and haptens, etc. A small organic molecule can provide a means for attachment of a nucleotide sequence to a label or to a support.

As used herein, a "support or surface" refers to a porous or non-porous water insoluble material. The support can be hydrophilic or capable of being rendered hydrophilic and includes inorganic powders such as silica, magnesium sulfate, and alumina; natural polymeric materials, particularly cellulosic materials and materials derived from cellulose, such as fiber containing papers, e.g., filter paper, chromatographic paper, etc.; synthetic or modified naturally occurring polymers, such as nitrocellulose, cellulose acetate, poly (vinyl chloride), polyacrylamide, cross linked dextran, agarose, polyacrylate, polyethylene, polypropylene, poly(4-methylbutene), polystyrene, polymethacrylate, poly(ethylene terephthalate), nylon, poly(vinyl butyrate), etc.; either used by themselves or in conjunction with other materials; glass available as Bioglass,

ceramics, metals, and the like. Natural or synthetic assemblies such as liposomes, phospholipid vesicles, and cells can also be employed.

Binding of sbp members to a support or surface may be accomplished by well-known techniques, commonly available in the literature. See, for example, "Immobilized Enzymes," Chibata, Halsted Press, New York (1978) and Cuatrecasas, J. Biol. Chem., 245:3059 (1970). The surface can have any one of a number of shapes, such as strip, rod, particle, including bead, and the like.

As used herein, a "label" refers to a member of a signal producing system. Labels include reporter molecules that can be detected directly by virtue of generating a signal, and specific binding pair members that may be detected indirectly by subsequent binding to a cognate that contains a reporter molecule such as oligonucleotide sequences that can serve to bind a complementary sequence or a specific DNA binding protein; organic molecules such as biotin or digoxigenin that can bind respectively to streptavidin and antidigoxin antibodies, respectively; polypeptides; polysaccharides; and the like. In general, any reporter molecule that is detectable can be used. The reporter molecule can be isotopic or nonisotopic, usually non-isotopic, and can be a catalyst, such as an enzyme, dye, fluorescent molecule, chemiluminescer, coenzyme, enzyme substrate, radioactive group, a particle such as latex or carbon particle, metal sol, crystallite, liposome, cell, etc., which may or may not be further labeled with a dye, catalyst or other detectable group, and the like. The reporter group can be a fluorescent group such as fluorescein, a chemiluminescent group such as luminol, a terbium chelator such as N-(hydroxyethyl) ethylenediaminetriacetic acid that is capable of detection by delayed fluorescence, and the like.

The label is a member of a signal producing system and can generate a detectable signal either alone or together with other members of the signal producing system. As mentioned above, a reporter molecule can serve as a label and can be bound directly to a nucleotide sequence. Alternatively, the reporter molecule can bind to a nucleotide sequence by being bound to an sbp member complementary to an sbp member that

comprises a label bound to a nucleotide sequence.

As used herein, a "signal producing system" refers to a system that may have one or more components, at least one component being the label. A signal producing system generates a signal indicative of the presence of a difference between the target polynucleotide sequence and the reference polynucleotide sequence. The signal producing system includes all of the reagents required to produce a measurable signal. When a reporter molecule is not conjugated to a nucleotide sequence, the reporter molecule is normally bound to an sbp member complementary to an sbp member that is bound to or part of a nucleotide sequence. Other components of the signal producing system can include substrates, enhancers, activators, chemiluminescent compounds, cofactors, inhibitors, scavengers, metal ions, specific binding substances required for binding of signal generating substances, coenzymes, substances that react with enzymatic products, enzymes and catalysts, and the like.

As used herein, "ancillary materials" refers to various ancillary materials that frequently may be employed in the methods and assays carried out in accordance with the present invention. For example, buffers will normally be present in the assay medium, as well as stabilizers for the assay medium and the assay components. Frequently, in addition to these additives, proteins may be included, such as albumins, organic solvents such as formamide, quaternary ammonium salts, polycations such as dextran sulfate, surfactants, particularly non-ionic surfactants, binding enhancers, e.g., polyalkylene glycols, or the like.

The phrase "consisting essentially of" when referring to a particular nucleotide or amino acid means a sequence having the properties of a given SEQ ID NO:. For example, when used in reference to an amino acid sequence, the phrase includes the sequence per se and molecular modifications that would not affect the basic and novel characteristics of the sequence.

As used herein, a nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. The term "operably linked" is frequently used to refer to a regulatory sequence capable of mediating the expression of a coding sequence and which is placed in a DNA molecule (e.g., an expression vector) in an appropriate position relative to the coding sequence so as to effect expression of the coding sequence. This same definition is sometimes applied to the arrangement of coding sequences and transcription control elements (e.g. promoters, enhancers, and termination elements) in an expression vector. This definition is also sometimes applied to the arrangement of nucleic acid sequences of a first and a second nucleic acid molecule wherein a hybrid nucleic acid molecule is generated. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. Enhancers do not, however, have to be contiguous to be operably linked. As described herein, PCR amplification may be used to operably link stretches of nucleic acid sequences in a resultant amplicon.

As used herein, the term "oncogene" refers to a genetic sequence whose expression within a cell promotes transformation processes in the cell and/or induces the cell to become a cancerous cell. Similarly, the term "proto-oncogene" is used herein to mean a genetic sequence, residing in the normal genome of a normal, non-cancerous cell, which has the potential, upon additional alterations or in the context of certain cellular milieu, to become an oncogene.

As used herein, a "first portion of a restriction endonuclease site" refers to a stretch of nucleic acid sequences comprising part of a larger stretch of nucleic acid sequences (i.e., restriction endonuclease site) recognized and cleaved by a restriction endonuclease.

As used herein, a "second portion of a restriction endonuclease site" refers to a stretch of nucleic acid sequences comprising part of a larger stretch of nucleic acid sequences (i.e., restriction endonuclease site) recognized and cleaved by a restriction endonuclease.

As used herein, the phrase “a first portion and second portion of a restriction endonuclease site operably linked by a PCR amplification” refers to a generation of a restriction enzyme site comprising a first and second portion, wherein the portions are linked or rendered contiguous by PCR amplification.

As used herein, the term “polymerase chain reaction (PCR) primer pair” refers to a first and a second primer of sufficient complementarity to a template nucleic acid sequence to hybridize to the template nucleic acid sequence at two physically separated sites and on separate strands such that extension from a first primer produces a single stranded nucleic acid which is at least partially complementary to a single stranded nucleic acid extended from a second primer.

As used herein, a “target nucleic acid sequence amplicon” refers to an at least partially double stranded nucleic acid sequence generated by PCR from a target nucleic acid sequence template.

As used herein, a “a pattern of nucleic acid fragments” refers to a plurality of nucleic acid sequences which are produced following, for example, digestion of a larger nucleic acid sequence with a restriction enzyme. Such fragments, therefore, comprise subportions of the larger nucleic acid sequence.

As used herein, “an allele associated with a disorder” refers to an allele comprising a nucleic acid variation or mutation that differs from that of a wild type allele and is associated and/or causatively linked to a disorder.

The basic molecular biology techniques used to practice the methods of the invention are well known in the art, and are described for example in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York; Ausubel et al., 1988, Current Protocols in Molecular Biology, John Wiley & Sons, New York; and Ausubel et al., 2002, Short Protocols in Molecular Biology, John Wiley & Sons, New York).

Catalogs pertaining to restriction enzymes of utility in the practice of the present invention are known to skilled artisans and a variety of such enzymes are listed in and commercially available through a number of catalogs, including, but not limited to: New England Biolabs 2002-2003 Catalog and Technical Reference, Published by New England Biolabs, 32 Tozer Road, Beverly, MA 01915-9965. Exemplary restriction enzyme sites incorporated into PCR amplicons generated from a template comprising a target nucleic acid sequence comprising a mutation are recognized by Alw26 I, Bcg I, and Sfu I. See Examples I and II.

Protocols pertaining to PCR methodology are provided in a number of laboratory manuals that are known to skilled practitioners and readily available. One such reference useful for the practice of the method of the invention is Goydos and Reintgen. A Molecular Technique Useful in the Detection of Occult Metastases in Patients with Melanoma: RT-PCR Analysis of Sentinel Lymph Nodes and Peripheral Blood. In Methods in Molecular Medicine Series, Melanoma, Nickoloff, BJ (ed.) The Humana Press Inc. Totowa, New Jersey 2001.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and described the methods and/or materials in connection with which the publications are cited.

As mentioned above, one aspect of the present invention concerns a method for detecting a difference in the nucleic acid sequence of two related nucleic acid sequences. In the method, the presence of such a difference is detectable by incorporation of a novel restriction enzyme site into PCR amplicons generated by amplification of a sequence comprising a mutation (which may be referred to herein as a target nucleic acid

sequence), but not into PCR amplicons generated by amplification of a sequence which does not comprise the mutation (which may be referred to herein as a reference nucleic acid sequence). Amplicons produced following PCR amplification of a plurality of nucleic acid sequence templates comprising target and reference nucleic acid sequences are subsequently digested with an enzyme which recognizes and cleaves the incorporated novel restriction enzyme site of target nucleic acid sequence amplicons. The identification of enzymatic fragments consistent with the presence of target nucleic acid sequence amplicons comprising the novel restriction enzyme site is indicative of the presence of a target nucleic acid sequence in the plurality of nucleic acid sequences. Thus, the method may be employed for detecting the presence of a target nucleic acid sequence in a sample.

Recent evidence suggests that specific defects in components of mitogen-activated protein kinase (MAPK) pathways may be responsible for the pathogenesis of the majority of human melanomas. Davies et al. recently reported that approximately 60% of melanomas have a mutation in *B-RAF* that leads to constitutive activation of MAPK pathways (Davies et al. *Nature* 2002; 417(6892):949-54). Mutations in *N-RAS*, an upstream component of this pathway, occur in approximately 25% of melanomas. These *B-RAF* and *N-RAS* mutations appear to be mutually exclusive (Davies et al., *supra*; Ball et al. *J Invest Dermatol* 1994; 102(3):285-90; Omholt et al. *Clin Cancer Res* 2002; 8(11):3468-74; Urquhart et al. *J Invest Dermatol* 2002; 119(3):556-561). Alterations in MAPK signaling may, therefore, play a role in the pathogenesis of the majority of melanomas, implying that the development of drugs that antagonize these changes could lead to improved therapies.

Only a small number of clinical melanoma specimens have been screened for MAPK pathway mutations, however, so the incidence of these mutations in human melanoma is therefore not yet known (Davies et al., *supra*). Accordingly, a clinically useful screening test for the presence of MAPK pathway mutations, which is rapid, sensitive and adaptable to different cell/tissue types that have been maintained and/or preserved by

different methods, would be useful for monitoring and stratifying patients undergoing MAPK pathway-targeted therapies.

To address the need for such a clinically useful screening test, the present inventors have developed a sensitive and specific screening assay for the presence of the three most common point mutations observed in molecules involved in MAPK pathways and found to be associated with human melanoma. Exemplary mutations of such MAPK pathway components include, but are not limited to, the V599E mutation of *B-RAF* and the Q61K and Q61R mutations of *N-RAS*. The method of the present invention was used effectively to determine the incidence of these mutations in melanoma specimens. The results presented herein validate the screening method of the invention and document the incidence of *B-RAF* and *N-RAS* mutations in human melanoma.

Table 1 provides a list of primer sequences used in Example I. It is to be understood that the method of the present invention is not limited to the use of the below listed primers.

Target	Primer	Sequence (SEQ ID NO:)	Anneal
Beta Actin	Forward	ATGAGATTGGCATGGCTTTA (1)	52° C
	Reverse	GGTGTGCACTTTTATTCAAC (2)	
Tyrosinase	Forward	TTGGCAGATTGTCTGTAGCC (3)	56° C
	Reverse	AGGCATTGTGCATGCTGCTT (4)	
MART-1	Forward	ATGCCAAGAGAAGATGCTCAC (5)	55° C
	Reverse	AGCATGTCTCAGGTGTCTCG (6)	
V599E <i>B-RAF</i>	Forward	ATGGATTACTTACACGCCAAGTCAATCATCCACAAAGACC TCA (7)	68° C
	Reverse	CAACTGTTCAAACCTGATGGGACCCACTCCATCGAGATGTC (8)	
Q61R <i>N-RAS</i>	Forward	ATGACTGAGTACAAACTGGTGGTGGTGGAGCAGG TGGTGTT (9)	68° C
	Reverse	GCCTGTCCTCATGTATTGCTGTCTCATGGCACTGCACTCT C (10)	
Q61K <i>N-RAS</i>	Forward	ATAGATGGTGAAACCTGTTTGGTGGACATACTGGATACAG TTCGA (11)	60° C
	Reverse	CGCTTAATCTGCTCCCTGTAGAGGTTAATAATC (12)	

SEQ ID NOs: are indicated by number in parentheses in Table 1. Primers are in 5' to 3' orientation.

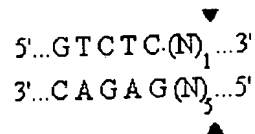
EXAMPLE I

MATERIALS AND METHODS

Detecting Point Mutations in Heterogeneous Tissues: As described herein, a strategy to detect point mutations in heterogeneous tissues containing both wild type (WT) and mutant *B-RAF* and *N-RAS* genes was devised. WT mRNA was anticipated to be present in every specimen because clinical melanoma specimens are likely to comprise normal cells (lymphocytes, fibroblasts, etc.), as well as transformed cells, in the tissue samples. Moreover, the melanoma cells are likely to be heterozygous for the *N-RAS* and *B-RAF* alleles. Thus, a method was developed which is capable of detecting a small copy number of mutant *B-RAF* and *N-RAS* alleles in a wild type background.

The method of the invention utilizes reverse transcriptase-polymerase chain reaction (RT-PCR) amplification followed by restriction enzyme digestion to detect point mutations when a mutant allele is present in a sample. As described herein, the methodological strategy involves incorporation of a specific restriction enzyme site into cDNA derived from an allele in which a mutation of interest is present. As a consequence, the presence of the incorporated restriction enzyme site only in PCR products amplified from mutant allele templates renders such PCR products sensitive to digestion with the restriction enzyme. Accordingly, digestion of the PCR products or amplicons (cDNA) with the restriction enzyme produces a pattern of identifiable fragments of predictable sizes, the appearance of which is indicative of the presence of a mutant allele in a sample. When a sample comprises only a WT allele, the restriction site is not incorporated into the amplified products and the diagnostic pattern of enzymatic fragments is not observed. Of note, restriction sites of the type incorporated in the methods of the invention are not normally present in the Q61R *N-RAS*, Q61K *N-RAS*, or the V599E *B-RAF* mutation sites. As shown herein, however, site-directed mutagenesis using specifically designed PCR primers can be used to introduce changes in sequences located near the point mutations so as to produce diagnostic restriction sites.

Detecting *B-RAF* V599E Mutation: The V599E mutation in *B-RAF* is produced by the substitution of an adenine for a thymine in codon 1796 (A1796T), the incorporation of which results in the substitution of a glutamic acid for a valine at position 599 of the encoded protein. Several restriction sites exist near codon 1796 in *B-RAF*. Alw26 I is a restriction enzyme that cuts the following sequence (arrows indicate the site cut, N = any nucleotide):



The top strand of the Alw26 I site 5'...GTCTC.(N)₁...3' is designated herein as SEQ ID NO: 13 and the bottom strand of the Alw26 I site 5'...(N)₃GAGAC...3' is designated herein as SEQ ID NO: 14. An Alw26 I restriction site spanning codons 574/575 naturally occurs in *B-RAF*. This restriction site was eliminated by site-directed mutagenesis using a forward primer. See Figure 1A and Table 1. A novel, diagnostic Alw26 I restriction was introduced into the V599E mutant *B-RAF* sequence by site directed mutagenesis using a reverse primer. See Figure 1A and Table 1. These primers produced a 150 bp product that was cut by Alw26 I into 123 bp and 37 bp fragments if the V599E mutation was present, but remained a 150 bp product if only the WT sequence was present. See Figure 1B. The digested PCR product was run on a 15% polyacrylamide gel and visualized using ethidium bromide staining. See Figure 1C.

Detecting *N-RAS* Q61R and Q61K Mutations: In that the two most common point mutations that result in constitutive activation of *N-RAS* in melanoma (Q61R and Q61K) do not form unique restriction sites, site-directed mutagenesis was used to produce restriction sites that could be used to advantage to identify these *N-RAS* mutations when present in a sample. Using site-directed mutagenesis of codon 64 of *N-RAS*, a Bcg I restriction site was incorporated specifically into PCR products amplified from mutant alleles comprising the Q61R mutation. The Bcg I site was not, however, incorporated

into PCR products amplified from either WT alleles or alleles comprising the Q61K mutation. See Figure 2A and Table 1. As shown below, Bcg I cuts the following sequence (arrows indicate the areas cut, N=any nucleotide):

5'... NNN NNN NNN NNN CGA NNN NNN TGC NNN NNN NNN N ...3'

The Bcg I site 5'...NNN NNN NNN NNN CGA NNN NNN TGC NNN NNN NNN N...3' is designated herein as SEQ ID NO: 15. Digestion of PCR products amplified from alleles which do not comprise the Q61R mutation with Bcg I produced a 34bp fragment, and cut at the 5' and 3' ends of the cDNA molecule. In contrast, digestion of PCR products amplified from Q61R alleles into which specific primers had been used to insert a nucleotide change, resulted in the generation of 168bp, 34bp, and 22bp Bcg I cleaved fragments of the 224bp PCR product. See Figure 2B and 2C.

To detect the Q61K mutation, an Sfu I restriction site was incorporated specifically into cDNA sequences comprising the Q61K mutation by using primers that change nucleotides in codons 59 and 60 of *N-RAS*. See Figure 3A. As shown below, Sfu I cuts the following sequence (arrows indicating the area cut):

5'...TTCGAA...3'

The top strand of the Sfu I site 5'...TTCGAA...3' is designated herein as SEQ ID NO: 16. Primers that insert the two nucleotide changes shown in Figure 3A produce a 250bp PCR product that is cut by Sfu I into 210bp and 40bp fragments if the Q61K mutation is present in *N-RAS*. See Figure 3B and 3C.

Sensitivity and Specificity: To test the sensitivity and specificity of this technique for identifying the V599E mutation, plasmids were constructed that contained either the WT *B-RAF* sequence or the V599E mutant sequence. Primers were designed that amplified a 300 bp segment of *B-RAF* cDNA centered around codon 1796. MCF-7 cells (known to

be *B-RAF* WT) (Davies et al. *supra*) were used to produce the cDNA for the WT plasmid and HT-144 melanoma cells (known *B-RAF* V599E mutant) (Davies et al. *supra*) were used to produce the cDNA for the mutant plasmid. These cDNAs were inserted into plasmids according to the manufacturer's protocol (Invitrogen). Plasmids were cloned and amplified in competent *E. coli*, and were sequenced using the sequencing primers supplied with the plasmid to verify the sequence. To determine the sensitivity and specificity of the V599E detection protocol, *B-RAF* sequence containing plasmids were serially diluted from 10^9 to 10 copies/reaction and these diluted solutions were used in the V599E detection protocol.

The sensitivity and specificity of the system for detecting *N-RAS* mutations was corroborated using essentially the same method as described above for detecting the *B-RAF* mutation. Briefly, plasmids were constructed that comprised either a WT *N-RAS* cDNA or one of the Q61 mutations. These *N-RAS*-containing plasmids were serially diluted from a concentration of 10^9 down to 10 copies/reaction. Plasmids comprising either WT or mutant sequences were also used in all experiments as positive and negative controls.

Western blotting: Cultured cells or homogenized frozen tissue specimens were lysed on ice for 45 minutes with RIPA buffer (10 mM sodium phosphate, pH 7.2, 1% nonidet P-40, 1% sodium deoxycholate, 0.1% SDS, 150 mM NaCl, 2 mM EDTA) supplemented with fresh 1% aprotinin, 1 mM phenylmethylsulfonyl fluoride, and 50 μ g/ml leupeptin, and centrifuged at 14,000 x g at 4°C for 10 minutes. Proteins were resolved by 10% SDS-PAGE and transferred to nitrocellulose membranes. The blots were incubated in blocking solution consisting of 5% milk in TBS-T (0.1% Tween-20) for 1 hour at 25°C, then immunoblotted with polyclonal anti-ERK antibody (Santa Cruz Biotechnology, Inc., Santa Cruz, CA) or anti-phospho-MEK antibody (Sigma, St Louis, MO). Detection by enzyme-linked chemiluminescence was performed according to the manufacturer's protocol (Amersham Pharmacia Biotech, Inc., Piscataway, NJ). Experiments were done under conditions of linearity with respect to protein concentration.

Clinical Melanoma Specimens: 85 melanoma samples were analyzed herein, which included primary tumors (25), regional dermal metastases (25), nodal metastases (25), and distant metastases (10). The Tissue Retrieval Service of the Cancer Institute of New Jersey banked these specimens, under a blanket IRB approved protocol, in a fashion that preserves patient confidentiality and conforms to HIPAA regulations. Each specimen was obtained in the operating room and snap frozen in liquid nitrogen within 5 minutes of resection. The specimens were stored at -80°C until processed. Total RNA was extracted from the specimens using a standard spin-column based system (RNAeasy, Qiagen) and first-strand synthesis was performed using a standard kit (Superscript First Strand Synthesis Kit, Invitrogen). All melanoma specimens used in this study were positive by PCR for beta actin (Ponte et al. *Nucleic Acids Res* 1984; 12(3):1687-96), tyrosinase (Brossart et al. *J. Invest. Dermatol.* 1993; 101(6):887-889; Goydos et al. *J Am Coll Surg* 1998; 187(2):182-190) and MART-1 (Goydos et al. *supra*; Reed and Albino. *Clin Lab Med* 2000; 20(4):817-38), the presence of which, respectively, confirmed RNA integrity and the presence in the specimen of melanoma cells.

Primers and PCR Conditions: The primers and PCR conditions used for the detection of beta-actin, tyrosinase, and MART-1, as well as the primers used in the site-directed mutagenesis detection protocol for the V599E *B-RAF* and the Q61 *N-RAS* mutations are shown in Table 1. PCR reactions (25 μl reactions) were run using a standard *Taq* polymerase (MasterTaq, Eppendorf), with an initial denaturing step at 94°C for 3 minutes followed by 40 cycles consisting of denaturing at 94°C for 30 seconds, annealing at the specific temperature for each set of primers for 30 seconds, and extension at 72°C for 1 minute. A final extension at 72°C for 8 minutes was followed by storage at 4°C . Restriction enzyme digestions were performed using 10 μl of the resultant PCR product at 36°C for two hours with the appropriate enzymes and buffers as per manufacturer's instructions. Digests were run on 15% polyacrylamide gels and visualized by ethidium bromide staining and UV transillumination. Controls included the use of known mutant and wild-type specimens in each run. BLAST searches confirmed that the primer sequences used in these reactions did not anneal to other known genes.

Statistical Analysis: The statistical analysis was performed at the Division of Biometrics at The Cancer Institute of New Jersey. Comparison of the incidence of the V599E point mutation in melanoma samples from different stages of progression was performed using contingency tables and the chi squared test, with P values less than 0.05 considered significant.

Specific Methodological Details Pertaining to the Drawings

In Figure 1A, an arrow indicates the thymine to adenine V599E point mutation. Changes introduced by the primers are shown in boxes. An adenine is substituted for guanine near the 3' end of the forward primer to eliminate an Alw26 I site that spans exons 574 and 575 in both the mutant and WT sequences. A substitution of a cytosine for an adenine in the reverse primer produces a new Alw26 I restriction site in the mutant sequence but not in the WT sequence. Figure 1B shows the resultant digestion products. Figure 1C shows a representative agarose gel electrophoresis result. L=ladder, Pos = positive control (HT-144 cell line), Neg = Negative control (MCF-7 cell line), lanes 1 - 5 are tumor samples. Tumor sample 3 shows cutting with Alw26 I demonstrating a V599E mutation of *B-RAF* in this tumor sample. A 160bp band is still seen after digestion of the PCR product from tumor sample 3 and most likely represents WT *B-RAF* sequence from contaminating normal cells in that sample.

In Figure 2A, the 3' end of the reverse primer introduced a change from a guanine to an adenine (box) in codon 64 to produce a Bcg I restriction site in the Q61R mutant cDNA that is not present in the WT or Q61K mutant cDNA. The forward primer binds to the first 40 nucleotides of the cDNA to produce a 224 bp PCR product that is cut by Bcg I into a 168 bp product, a 34 bp product, and a 22 bp product if the sequence contains the Q61R mutation, but remains as a 224 bp product if the sequence contains the Q61K mutation (see Figure 4) or is WT. Figure 2A shows the resultant digestion products. Figure 2C shows a representative agarose gel electrophoresis result. L=ladder, lane 1 = positive control (SK-Mel 2 cell line), lane 2 = negative control (MCF-7 cell line), lanes 3 - 7 are tumor samples. Tumor samples 5 and 6 show cutting with Bcg I demonstrating a Q61R mutation of *N-RAS* in these two tumor samples (34 bp band is very faint at bottom

of gel and 22 bp band is not shown). A 224bp band was still seen after digestion of the PCR product from tumor samples 5 and 6 that most likely represented WT *N-RAS* sequence from normal cells present in the sample.

In Figure 3A, the 5' end of the forward primer introduces a change of a thymine to a cytosine and a cytosine for a guanine (boxes) in codons 59 and 60 to produce an Sfu I restriction site in the Q61K mutant that was not present in the WT or Q61R mutant. The reverse primer binds downstream to produce a 250 bp PCR product that is cut by Sfu I into a 210 bp product and a 40 bp product if the sequence contains the Q61K mutation but remains as a 250 bp product if the sequence comprises the Q61R mutation or is WT. Figure 3B shows the resultant digestion products. Figure 3C shows a representative agarose gel electrophoresis result. L = ladder, Neg = negative control (MCF-7 cell line), Pos = positive control, lanes 1 - 9 are tumor samples. Tumor sample 9 shows cutting with Sfu I demonstrating a Q61K mutation of *N-RAS* in this tumor sample (40 bp band is not shown). A 250bp band is still seen after digestion of the PCR product from tumor sample 9 that most likely represents WT *N-RAS* sequence from contaminating normal cells in that sample.

In Figure 4, serial dilutions of plasmids range from 10^6 to 10 copies per reaction. L = Ladder, 0 = no plasmid in the reaction. A 123 bp band is visible at a concentration as low as 10^2 plasmids per reaction.

Figure 5A shows a Western blot of protein samples extracted from cell lines with either WT *N-RAS* and *B-RAF* or a mutation in one or the other of these genes. Antibodies against ERK 1/2 (upper panel) or MEK 1/2 (lower panel) were used. SK-Mel 31 melanoma cells (lane 2) and HUVEC cells (lane 6) are known to be WT for both *N-RAS* and *B-RAF* and are used as the baseline level of phosphorylated MEK and ERK. A2058 melanoma cells (lane 3), HT-144 melanoma cells (lane 4), and MEL 501 melanoma cells (lane 5) have known V599E *B-RAF* mutations and showed varying degrees of increased levels of phosphorylated MEK and ERK over baseline. SK-Mel 2 cells (lane 1) have a known *N-RAS* mutation (Q61R) and showed a similar increase in the phosphorylated

forms of MEK and ERK as the cell lines with V599E *B-RAF* mutations. Arrows indicate the two bands representing ERK1 and 2 (upper panel) and the two bands that represent MEK1 and 2 (lower panel). Loading controls were run demonstrating equal protein loading in each lane (not shown).

Figure 5 B shows a Western blot using protein extracted from 7 human melanoma specimens. Tumors 1-3 were found to be WT in both *B-Raf* and *N-Ras* and show little increase in the phosphorylated forms of ERK 1 and 2. Tumors 4 and 5 were found to harbor the V599E *B-Raf* mutation and each showed increased phosphorylation of ERK 1 and 2. Tumor 6 harbors a Q61K *N-Ras* mutation and Tumor 7 harbors a Q61R *N-Ras* mutation and both demonstrated an increase in the phosphorylated forms of ERK 1 and 2. Lane 8 is a negative control (MCF-7 cell line) and lane 9 a positive control (HT-144 cell line, known V599E mutant). Total ERK 1 and 2 staining demonstrates that increases in total ERK 1 and 2 did not account for the increase observed in the phosphorylated forms.

RESULTS

Determining the Sensitivity and Specificity of Site-directed Mutagenesis: To determine sensitivity and specificity of the site-directed mutagenesis procedure on plasmids containing either mutant or WT *B-RAF* cDNA, solutions comprising these cDNAs were serially diluted from 10^9 to 10 copies/reaction and tested as described herein. Figure 4 demonstrates that as few as 100 copies of mutant *B-RAF* sequence were detectable using the method of the invention. Moreover, up to 10^{11} copies per reaction of WT sequence produced no detectable mutant-specific bands when digested with Alw26 I (data not shown). Using the same method, plasmids that contained either a WT *N-RAS* cDNA or one of the Q61 mutations were tested, and as few as 100 copies of either the Q61R or the Q61K mutation were detectable. Furthermore, no detectable mutant-specific band was produced when amplification products generated from as many as 10^{11} copies of WT sequence PCR template per reaction were digested with Sfu I or Bcg I (data not shown).

Incidence of *B-RAF* and *N-RAS* Mutations in Melanoma: The site-directed mutagenesis technique of the present invention was used to detect V599E *B-RAF* mutations and the Q61K and Q61R *N-RAS* mutations in 85 clinical melanoma samples. As shown herein, 33 of the 85 samples (7 of 25 primary tumors, 15 of 25 regional dermal metastases, 5 of 25 nodal metastases, and 6 of 10 distant metastases) had the V599E mutation (39 %). None of the samples positive for a V599E mutation comprised either a Q61K or Q61R *N-RAS* mutation. Of the 85 samples tested, 17 (20%) contained an *N-RAS* mutation (5 primary tumors, 7 regional dermal metastases, 3 nodal metastases, and 2 distant metastasis), 12 contained a Q61R mutation and 5 contained a Q61K mutation. Thus, either an *N-RAS* or *B-RAF* mutation was detected in 50 of 85 samples tested (59%). Thirty-five of the 85 melanoma samples analyzed herein contained neither the Q61 *N-RAS* mutation nor the V599E *B-RAF* mutation (41 %). There was a significant difference in the incidence of the V599E *B-RAF* mutation in melanoma samples representing different stages of disease progression. Indeed, regional dermal metastatic lesion and distant metastases had a significantly higher incidence of the V599E mutation than that observed for primary tumors or nodal metastatic lesions ($p < 0.01$).

Downstream Effects of Activating MAPK Mutations in Cell Lines: Anti-phospho-MEK and ERK antibodies (Kolch. *Biochem J* 2000; 351 Pt 2:289-305; Lee and McCubrey. *Leukemia* 2002; 16(4):486-507; Marais and Marshall. *Cancer Surv* 1996; 27:101-25; Peyssonnaud and Eychene. *Biol Cell* 2001; 93(1-2):53-62) were used to detect MAPK activation in cell lines known to be WT for *N-RAS* and *B-RAF* (HUVEC cells, and SK-Mel 31 melanoma cells; Davies et al. *supra*), mutant in *N-RAS* (SK-MEL 2 melanoma cell line; Davies et al. *supra*), or mutant for the V599E *B-RAF* mutation (HT-144, Mel 501, and A2058 melanoma cell lines; Daviès et al. *supra*). The level of phosphorylation of MEK and ERK in WT cell lines examined was considered the baseline level. As shown in Figure 5A, mutant cell lines had different elevated expression levels of phosphorylated MEK and ERK as compared to those of WT cell lines.

Downstream Effects of Activating MAPK Mutations in Clinical Specimens: The above-mentioned anti-phospho-ERK antibodies were also used to detect MAPK activation in clinical melanoma specimens. See Figure 5B. As shown herein, relative increases in phosphorylated forms of ERK in melanoma samples comprising V599E *B-RAF* or one of the two Q61 *N-RAS* mutations were observed as compared to those of specimens comprising only WT alleles.

DISCUSSION

As described herein, 39% of the clinical melanoma specimens tested harbored a V599E *B-RAF* mutation and 20% harbored one of the two known Q61 *N-RAS* mutations, thus demonstrating that approximately 60% of melanomas comprise one of these mutations. The incidence of *N-RAS* mutations in this study corroborated results described in previous reports (Ball et al. *J Invest Dermatol* 1994; 102(3):285-90). The incidence of the V599E *B-RAF* mutation presented herein was lower than reported by Davies et al who found that 5 of 9 melanoma specimens and 11 of 15 short-term melanoma cultures contained the V599E mutation (Davies et al. *supra*). The present analysis, however, involves a significantly larger number of melanoma specimens, and includes specimens from different states of disease progression. Thus, the present study presents a more comprehensive and, therefore, predictive assessment of the association/correlation of the presence of such mutant alleles with melanoma and disease progression.

As described herein, primary tumors (7 of 25) and nodal metastasis (5 of 25) had a lower incidence of the V599E mutation than did regional dermal metastases (15 of 25) or distant metastases (6 of 10) ($p < 0.01$). These data suggest that MAPK pathway mutations may be found at different rates in tumors representing different stages of progression and indicate that the different mutations impart different characteristics to a melanoma cell. Moreover, sixty percent of distant metastatic lesions in the present study contained a V599E mutation and 20% contained an *N-RAS* mutation, thereby suggesting that distant metastases have the highest incidence of mutations in MAPK pathway components.

These data were corroborated by the observation of an increase in the phosphorylation levels of downstream components/molecules of the MAPK pathway in transformed cells. As shown herein, a significant increase in phosphorylation levels of MEK and ERK was observed in cell lines and melanoma specimens that comprised one of the MAPK mutations (see Figure 5), suggesting that functional up-regulation of this pathway (Kolch. *Biochem J* 2000; 351 Pt 2:289-305; Lee and McCubrey. *Leukemia* 2002; 16(4):486-507; Marais and Marshall. *Cancer Surv* 1996; 27:101-25; Peyssonnaud and Eychene. *Biol Cell* 2001; 93(1-2):53-62) occurs in the MAPK mutated specimens.

The results presented herein suggest that activating mutations in the MAPK pathway play a prominent role in the development of melanoma. Therefore, targeting this pathway with specific therapeutic regimens is an important clinical goal. Clinical trials will require a specific and sensitive method to detect these mutations. Sequencing to detect such mutations, however, is expensive, time consuming, and requires sophisticated equipment and trained staff and personnel. Single-strand conformation polymorphism (SSCP) and denaturing gradient gel electrophoresis (DGGE) are two other methods used to detect gene mutations in tumor specimens. The sensitivity and specificity of SSCP and DGGE, however, are questionable and the necessity of confirming the presence of the mutation by sequencing limits the usefulness of these methods (Campos et al. *Clin Chem Lab Med* 2001; 39:401-404; Nedergaard et al. *Int J Cancer* 1997; 71:364-369; Pogue et al. *Genomics* 1998; 54:1-4). Detecting the mutant protein with specific antibodies using either immunohistochemical or Western blotting techniques is also useful. Immunohistochemistry is particularly useful for the simplified screening of archival, paraffin-embedded specimens. Immunohistochemical and immunoblotting approaches are limited, however, by the availability of diagnostic antibodies and technical expertise required to perform the assays accurately.

Herein is described a new method for screening to detect MAPK mutations which is based on the creation of a new diagnostic restriction site in amplicons generated by PCR amplification of either mutant *B-RAF* and *N-RAS* alleles. The method of the present invention is novel, sensitive, specific, simple, and inexpensive. Moreover, multiple

samples can be screened readily, thus lending the methodology to high throughput screening approaches. Such qualities render this method suitable for use in analysis of clinical specimens, in which tissue is limited and comprises a mixture of tumor and normal cells.

Treatment protocols that target MAPK pathway components have been examined in many different tumor types (Lee and McCubrey. *Leukemia* 2002; 16(4):486-507; Lyons et al. *Endocr Relat Cancer* 2001; 8(3):219-25; Midgley and Kerr. *Crit Rev Oncol Hematol* 2002; 44(2):109-20; Nottage and Siu. *Curr Pharm Des* 2002; 8(25):2231-42; Sebolt-Leopold. *Oncogene* 2000; 19(56):6594-9). Many of the methods that have been used to target this pathway in other cancer types may soon be tested in patients with melanoma. It will thus be important to be able to stratify patients by MAPK component mutation status in these protocols. The site-directed mutagenesis method of the present invention addresses this need.

EXAMPLE II

The method of the present invention, which utilizes a modified site-directed mutagenesis approach to detect mutations in heterogeneous tissues, may also be used to advantage to detect mutations in archival tissues. For such applications, genomic DNA from the sample is utilized as template for PCR amplification. The ability to use the method of the present invention in the context of archival tissue (e.g., paraffin-embedded tissue) greatly expands the utility of the method because large banks of such material are available for analysis. Moreover, DNA is much more stable than RNA and can survive intact in paraffin-embedded specimens.

Accordingly, the method of the present invention was used to analyze nucleic acid sequences isolated from paraffin-embedded melanoma specimens. The paraffin-embedded melanoma tumor samples analyzed were prepared in parallel from the same tissue samples that were flash-frozen and screened for MAPK pathway point mutations in Example I. Thus, the results produced using archival tissue as starting material are corroborated by and are corroborative of those results generated using flash frozen tissue.

Briefly, paraffin-embedded tumor samples were dewaxed using a standard method involving elevated temperature that is well known to those of skill in the art. Dewaxed tissue was placed in an Eppendorf tube and digested with proteinase K at 56°C overnight. Genomic DNA was extracted from the digested tissue with phenol and precipitated with ethanol in the presence of glycogen. PCR was performed using total genomic DNA and the Alw26 I site-directed mutagenesis primers described hereinabove. The resultant PCR products (i.e., amplicon) were cut with Alw26 I at 37°C for two hours and analyzed on a 15% polyacrylamide gel, which was stained with ethidium bromide to visualize the nucleic acid sequence fragments present in the PCR mix. For this analysis, melanoma samples known to be wild type for B-Raf (comprising only reference nucleic acid sequence) and samples known to comprise the V599E mutation (target nucleic acid sequence) were tested. In brief, the method of the invention was used successfully to detect the V599E mutation in all of the positive samples and did not register any false positive results for the samples known to be wild type at the codon encoding amino acid residue 599. Thus, the method of the present invention may be used to advantage for detecting mutations in nucleic acid sequences derived from archival tissue. ~

EXAMPLE III

The method of the present invention has been modified to address applications in which an overwhelming excess of wild type nucleic acid sequences in a sample renders detecting a small number of nucleic acid sequences comprising a mutation difficult. The excess of wild type nucleic acid sequences in the sample appears to decrease the level of amplification of the minority mutated nucleic acid sequences. To increase the sensitivity of the method of the invention under such conditions, a two-step method was developed.

In the first step, the amount of wild type amplicon/cDNA produced by PCR (i.e., cDNA generated by amplification from a wild type template) was reduced by selective digestion using a second restriction enzyme. To achieve this end for samples wherein detection of the V599E *B-RAF* mutation was the objective, a reverse primer was designed such that its incorporation not only produced a new Alw26 I restriction site in mutant amplicons, but

also a new Tsp45 I site in wild type amplicons. Tsp45 I cuts the following sequence (arrows indicate area cut, S = C or G):



The top and bottom strand of the Tsp45 I site are identical 5'...GTSAC...3' and are designated herein as SEQ ID NO: 17. As illustrated above, the original reverse primer used to produce the Alw26 I site in amplicons generated from the V599E mutant *B-RAF* produced a Tsp45 I restriction site in wild type *B-RAF* amplicons. See diagram hereinbelow. To capitalize on this feature, a forward primer that binds upstream relative to that of the binding site for the forward primer of the *B-RAF* sequence described in Example I was designed. When used with the original Alw26 I reverse primer, this forward primer produces a 407 bp cDNA/amplicon. Amplicons generated from wild type nucleic acid sequence templates are digested by Tsp45 I to generate fragments of 365 bp and 42 bp, whereas amplicons generated from mutant nucleic acid sequence templates were not digested by Tsp45 I and remained intact (407 bp). See diagram hereinbelow.

In brief, PCR amplifications were performed using the Tsp45 I forward and Alw26 I reverse primers to produce amplicons that were subsequently digested with Tsp45 I at 65°C for 2 hours. This initial digestion cuts the wild type amplicons/cDNA into smaller segments, and yet preserves V599E mutant amplicons, thus providing a means to select for mutant amplicons as intact and functional templates for a second PCR amplification. A second PCR was subsequently performed using the Tsp45 I digested PCR products as templates for extension/amplification and the Alw26 I forward and reverse primers. The fragmented wild type amplicons were not amplified by this second PCR reaction, allowing for selective amplification of the intact V599E mutant amplicons. Using this two-step technique, as few as 500 cells comprising V599E mutant encoding nucleic acid sequences were detectable, even when admixed with 10⁶ wild type cells. Similar two-step methods have been developed to detect mutant Q61R and Q61K *N-RAS* mutant cells in the face of overwhelming excess of wild type cells.

Diagrammatic representation of this exemplification of the invention:

5'...GGTCTAGCTACAGTGAAATCT...3'
 GTGAC

New Tsp45I restriction site produced by the reverse
 primer only in the wild type cDNA

While certain of the preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications may be made thereto without departing from the scope and spirit of the present invention, as set forth in the following claims.

CLAIMS

1. A method for detecting a mutation in a target nucleic acid sequence, said method comprising:

- (a) providing a plurality of nucleic acid sequences comprising said target nucleic acid sequence, wherein said mutation is located in a first portion of a restriction endonuclease site;
- (b) providing a first primer hybridizable to said target nucleic acid sequence, said first primer comprising a second portion of said restriction endonuclease site, and a second primer hybridizable to said target nucleic acid sequence, wherein said first and second primer comprise a polymerase chain reaction (PCR) primer pair;
- (c) performing a PCR amplification of said plurality of nucleic acid sequences using said PCR primer pair, wherein said PCR amplification produces a target nucleic acid sequence amplicon comprising a site recognizable by a restriction endonuclease in the presence of said mutation, said site comprising the first portion and second portion of said restriction endonuclease site, said first portion and second portion of said restriction endonuclease site operably linked by said PCR amplification;
- (d) incubating PCR amplicons produced in step (c) with said restriction endonuclease capable of recognizing said restriction endonuclease site under conditions permissible for said restriction endonuclease activity;
and
- (e) detecting nucleic acid fragments produced in step (d), wherein detection of a pattern of nucleic acid fragments is indicative of a

presence of said target nucleic acid sequence amplicon comprising a site recognizable by said restriction endonuclease, said pattern of nucleic acid fragments being indicative of a presence of a mutation in said target nucleic acid sequence in said plurality of nucleic acid sequences.

2. The method of claim 1, wherein said target nucleic acid sequence is an allele associated with a disorder.
3. The method of claim 1, wherein said target nucleic acid sequence is an oncogene or a proto-oncogene.
4. The method of claim 1, wherein said plurality of nucleic acid sequences comprising said target nucleic acid sequence is isolated from a biological sample.
5. The method of claim 4, wherein said biological sample is a patient sample.
6. The method of claim 1, wherein said presence of said mutation in said target nucleic acid sequence is indicative of a disorder or a predisposition to a disorder.
7. The method of claim 6, wherein said disorder is selected from the group consisting of a genetic disease, a metabolic disease, and hyperproliferative disease.
8. The method of claim 7, wherein said hyperproliferative disease is a cancer.
9. The method of claim 6, wherein said predisposition to a disorder is selected from the group consisting of a predisposition to a genetic disease, a metabolic disease, and hyperproliferative disease.
10. The method of claim 9, wherein said hyperproliferative disease is a cancer.

11. The method of claim 3, wherein a mutation in said oncogene is an activating point mutation.
12. The method of claim 3, wherein said oncogene is a *B-RAF* allele comprising a mutation or an *N-RAS* allele comprising a mutation.
13. The method of claim 12, wherein said mutation in a *B-RAF* allele encodes a mutated *B-RAF* polypeptide comprising a V599E mutation.
14. The method of claim 13, wherein said PCR primer pair comprises a first primer SEQ ID NO: 7 and a second primer SEQ ID NO: 8.
15. The method of claim 14, wherein said site recognizable by said restriction endonuclease is an Alw26 I site.
16. The method of claim 15, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Alw26 I comprises fragments of 123 and 37 base pairs.
17. The method of claim 16, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
18. The method of claim 12, wherein said mutation in an *N-RAS* allele encodes a mutated *N-RAS* polypeptide comprising a Q61R mutation.
19. The method of claim 18, wherein said PCR primer pair comprises a first primer SEQ ID NO: 9 and a second primer SEQ ID NO: 10.
20. The method of claim 19, wherein said site recognizable by said restriction endonuclease is a Bcg I site.

21. The method of claim 20, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Bcg I comprises fragments of 168, 34, and 22 base pairs.
22. The method of claim 21, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
23. The method of claim 12, wherein said mutation in an *N-RAS* allele encodes a mutated *N-RAS* polypeptide comprising a Q61K mutation.
24. The method of claim 23, wherein said PCR primer pair comprises a first primer SEQ ID NO: 11 and a second primer SEQ ID NO: 12.
25. The method of claim 24, wherein said site recognizable by said restriction endonuclease is an Sfu I site.
26. The method of claim 25, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Sfu I comprises fragments of 210 and 40 base pairs.
27. The method of claim 26, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
28. A method for detecting a mutation in a target nucleic acid sequence, said method comprising incorporating a restriction enzyme site into a target nucleic acid sequence amplicon, wherein said incorporating is effectuated by polymerase chain reaction (PCR) of a target nucleic acid sequence comprising a mutation, wherein said restriction enzyme site incorporated by PCR comprises said mutation in said target nucleic acid sequence amplicon, and said target nucleic acid sequence amplicon comprising the restriction enzyme site is digestable by said restriction enzyme, and digesting with said restriction

enzyme produces a pattern of nucleic acid fragments indicative of a presence of a target nucleic acid sequence comprising a mutation.

29. A method for diagnosing a disorder associated with a mutation in a target nucleic acid sequence, said method comprising:

- (a) providing a plurality of nucleic acid sequences comprising said target nucleic acid sequence, wherein said mutation is located in a first portion of a restriction endonuclease site;
- (b) providing a first primer hybridizable to said target nucleic acid sequence, said first primer comprising a second portion of said restriction endonuclease site, and a second primer hybridizable to said target nucleic acid sequence, wherein said first and second primer comprise a polymerase chain reaction (PCR) primer pair;
- (c) performing a PCR amplification of said plurality of nucleic acid sequences using said PCR primer pair, wherein said PCR amplification produces a target nucleic acid sequence amplicon comprising a site recognizable by a restriction endonuclease in the presence of said mutation, said site comprising the first portion and second portion of said restriction endonuclease site, said first portion and second portion of said restriction endonuclease site operably linked by said PCR amplification;
- (d) incubating PCR amplicons produced in step (c) with said restriction endonuclease capable of recognizing said restriction endonuclease site under conditions permissible for said restriction endonuclease activity;
and

(e) detecting nucleic acid fragments produced in step (d), wherein detection of a pattern of nucleic acid fragments is indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by said restriction endonuclease, said pattern of nucleic acid fragments being indicative of a presence of a mutation in said target nucleic acid sequence in said plurality of nucleic acid sequences, wherein said presence of said mutation is a positive diagnostic indicator of a disorder associated with said mutation in said target nucleic acid sequence.

30. The method of claim 29, wherein said target nucleic acid sequence is an allele associated with a disorder.

31. The method of claim 29, wherein said target nucleic acid sequence is an oncogene or a proto-oncogene.

32. The method of claim 29, wherein said plurality of nucleic acid sequences comprising said target nucleic acid sequence is isolated from a biological sample.

33. The method of claim 32, wherein said biological sample is a patient sample.

34. The method of claim 29, wherein said presence of said mutation in said target nucleic acid sequence is a positive indicator of a disorder or a predisposition to a disorder.

35. The method of claim 34, wherein said disorder is selected from the group consisting of a genetic disease, a metabolic disease, and hyperproliferative disease.

36. The method of claim 35, wherein said hyperproliferative disease is a cancer.

37. The method of claim 34, wherein said predisposition to a disorder is selected from the group consisting of a predisposition to a genetic disease, a metabolic disease, and hyperproliferative disease.
38. The method of claim 37, wherein said hyperproliferative disease is a cancer.
39. The method of claim 31, wherein a mutation in said oncogene is an activating point mutation.
40. The method of claim 31, wherein said oncogene is a *B-RAF* allele comprising a mutation or an *N-RAS* allele comprising a mutation.
41. The method of claim 40, wherein said mutation in a *B-RAF* allele encodes a mutated *B-RAF* polypeptide comprising a V599E mutation.
42. The method of claim 41, wherein said PCR primer pair comprises a first primer SEQ ID NO: 7 and a second primer SEQ ID NO: 8.
43. The method of claim 42, wherein said site recognizable by said restriction endonuclease is an Alw26 I site.
44. The method of claim 43, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Alw26 I comprises fragments of 123 and 37 base pairs.
45. The method of claim 44, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
46. The method of claim 40, wherein said mutation in an *N-RAS* allele encodes a mutated *N-RAS* polypeptide comprising a Q61R mutation.

47. The method of claim 46, wherein said PCR primer pair comprises a first primer SEQ ID NO: 9 and a second primer SEQ ID NO: 10.
48. The method of claim 47, wherein said site recognizable by said restriction endonuclease is a Bcg I site.
49. The method of claim 48, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Bcg I comprises fragments of 168, 34, and 22 base pairs.
50. The method of claim 49, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
51. The method of claim 40, wherein said mutation in an *N-RAS* allele encodes a mutated *N-RAS* polypeptide comprising a Q61K mutation.
52. The method of claim 51, wherein said PCR primer pair comprises a first primer SEQ ID NO: 11 and a second primer SEQ ID NO: 12.
53. The method of claim 52, wherein said site recognizable by said restriction endonuclease is an Sfu I site.
54. The method of claim 53, wherein said pattern of nucleic acid fragments indicative of a presence of said target nucleic acid sequence amplicon comprising a site recognizable by Sfu I comprises fragments of 210 and 40 base pairs.
55. The method of claim 54, wherein detection of said pattern of nucleic acid fragments is a positive indicator of melanoma.
56. The method of claim 17, 22, 27, 45, 50, or 55, wherein said detection of said pattern of nucleic acid fragments is an indicator of melanoma disease progression.

ABSTRACT

The present invention is directed to a novel method for detecting a mutation in a target nucleic acid sequence. Such methods may be used to detect a mutation in a target nucleic acid sequence derived from a biological sample. Exemplary biological samples include, but are not limited to, samples derived from patients such as bodily fluids, tissues or cells. The methods of the invention are useful for detecting a mutation in a target nucleic acid sequence in such patient samples and thus, are of utility for diagnosing a disease in a patient and/or predicting a predisposition of a patient for a disease.

FIGURE 1A

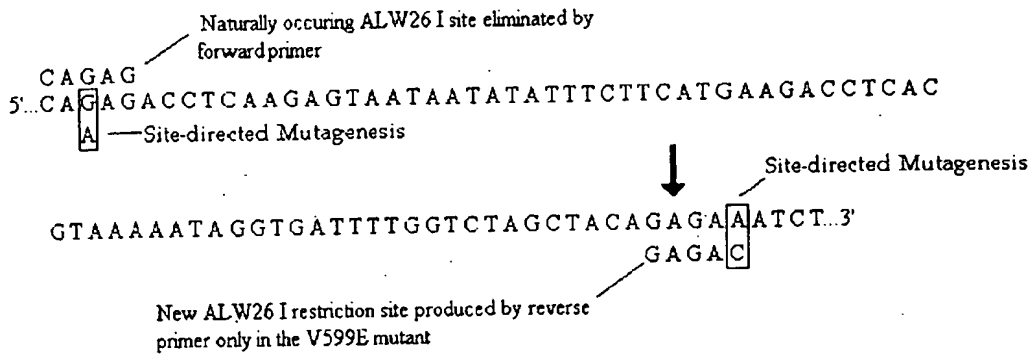


FIGURE 1B

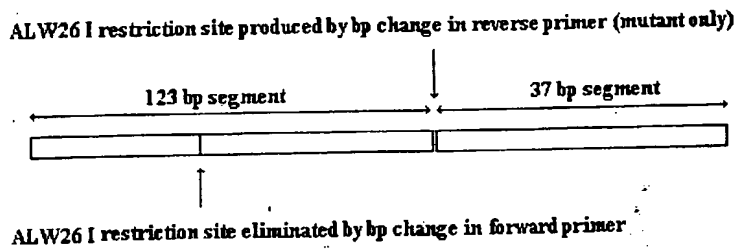


FIGURE 1C

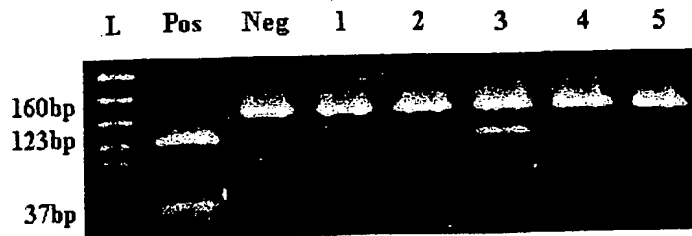


FIGURE 2A

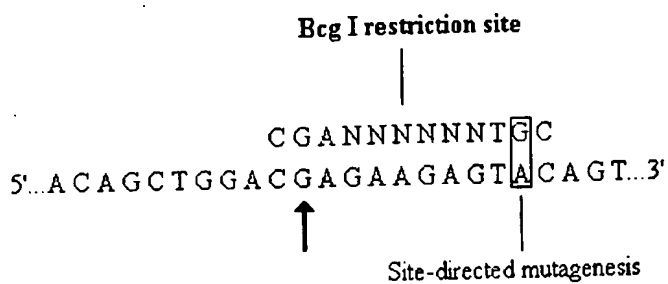


FIGURE 2B

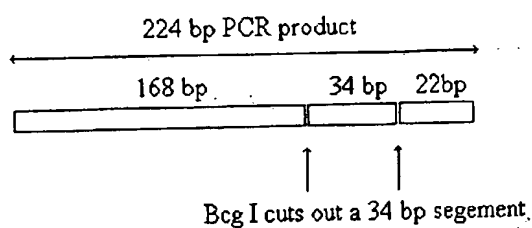


FIGURE 2C

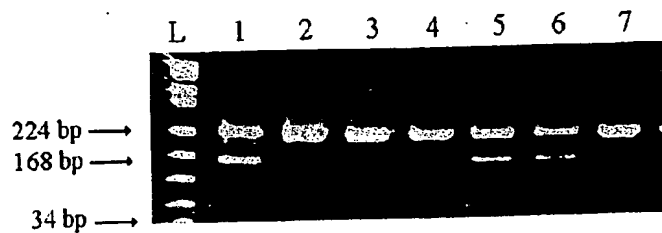


FIGURE 3A

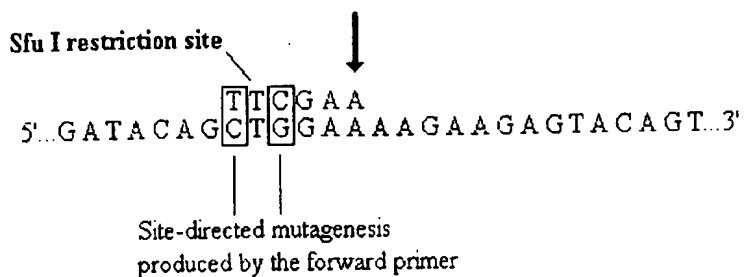


FIGURE 3B

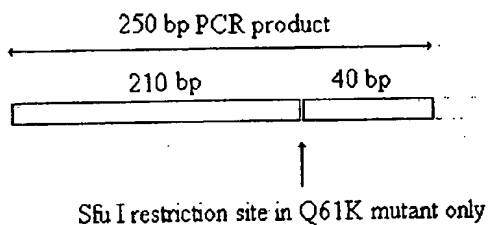


FIGURE 3C

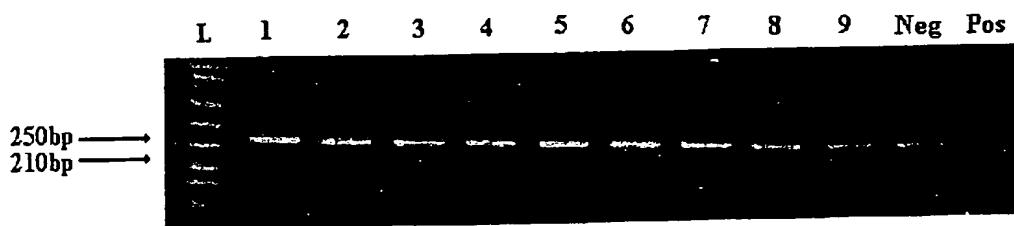


FIGURE 4

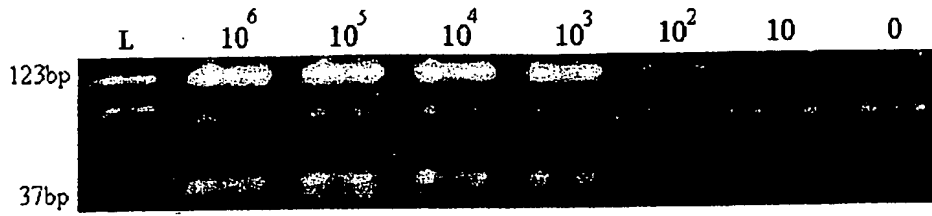


FIGURE 5A

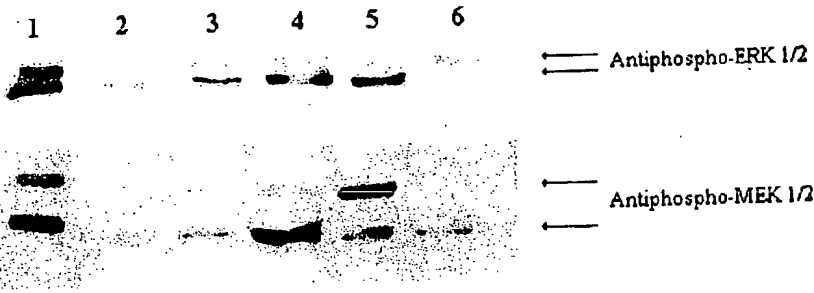


FIGURE 5B

